What is claimed is:

1.   A method of determining the genotype at a locus within genetic material obtained from a biological sample, the method comprising:

A.   reacting the material at the locus to produce a first reaction value indicative of the presence of a given allele at the locus;

B.   forming a data set including the first reaction value;

C.   establishing a distribution set of probability distributions, including at least one distribution, associating hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

D.   applying the first reaction value to each pertinent probability distribution to determine a measure of the conditional probability of each genotype of interest at the locus; and

E.   determining the genotype based on the data obtained from step (D).

2.   A method according to claim 1, wherein the distribution set includes a plurality of probability distributions for a corresponding plurality of genotypes of interest.

3.   A method, according to claim 1, further comprising:

(i) reacting the material at the locus to produce a second reaction value independently indicative of the presence of a second allele at the locus;

(ii) forming a second data set including the second reaction value; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

4. A method according to claim 2, further comprising:

(i) reacting the material at the locus to produce a second reaction value;

(ii) applying the first and second reaction values to each pertinent distribution to determine the probability of each genotype at the locus; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

5. A method according to claim 3, wherein each probability distribution associates a hypothetical pair of first and second reaction values with a single probability of each genotype of interest.

6. A method according to claim 4, wherein each probability distribution associates a hypothetical pair of

first and second reaction values with a single probability of each genotype of interest.

7. A method according to claim 1, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

8. A method according to claim 2, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

9. A method according to claim 3, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions

comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values in the first and second data sets.

10. A method according to claim 4, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values in the first and second data sets.

11. A method, according to claim 1, of determining the genotype at a locus within genetic material obtained from each of a plurality of samples, the method further comprising:

(1) performing step (A) with respect to the locus of material obtained from each sample;

(2) in step (B), including in the data set reaction values obtained from each sample.

12. A method according to claim 7, of determining the genotype of selected loci within genetic material obtained from a sample, the method further comprising:

(1) performing step (A) at each of the selected loci;

(2) in step (B), including in the data set reaction values obtained from each of the selected loci.

13. A method according to claim 7, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(2) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

(3) using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data set.

14. A method according to claim 8, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

5   (2)   using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

          (3)   using the results of step (2) to modify the initial probability distributions, so that the modified

10   distributions more accurately reflect the reaction values in the data set.

          15.   A method according to claim 9, wherein step (C) includes:

15   (1)   establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

          (2)   using the initial probability distributions to determine measures of the initial conditional probability

20   for each genotype at the locus; and

          (3)   using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in

25   the data set.

          16.   A method according to claim 10, wherein step (C) includes:

          (1)   establishing a set of initial probability

30   distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(2) using the initial probability distributions to determine initial conditional probabilities for each genotype at the locus; and

(3) using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data.

17. A method according to claim 13, wherein step (C) further includes:

(4) repeating steps (1) through (3) a desired number of times.

18. A method according to claim 14, wherein step (C) further includes:

(4) repeating steps (1) through (3) a desired number of times.

19. A method according to claim 15, wherein step (C) further includes:

(4) repeating steps (1) through (3) a desired number of times.

20. A method according to claim 16, wherein step (C) further includes:

(4) repeating steps (1) through (3) a desired number of times.

21.   A method according to claim 1, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data obtained from step (D).

22.   A method according to claim 3, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data obtained from step (D).

23.   A method according to claim 7, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data from step (D), the method further comprising (F) determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

24.   A method according to claim 9, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data from step (D), the method further comprising (F) of determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

25.   A method according to claim 1, wherein each allele is a single specific nucleotide.

26. A method according to claim 4, wherein each allele is a single nucleotide.

27. A method according to claim 1, wherein each allele consists of at least two specific nucleotides.

28. A method according to claim 4, wherein each allele consists of at least two specific nucleotides.

29. A method according to claim 1, wherein each allele is defined at least in part by its length in nucleotides.

30. A method according to claim 4, wherein each allele is defined at least in part by its length in nucleotides.

31. A method according to claim 1, wherein each allele is defined by one of the presence and absence of at least one restriction site.

32. A method according to claim 4, wherein each allele is defined by one of the presence and absence of at least one restriction site.

33. A method according to claim 4, wherein step (B) includes the step of including in the data set reaction values from prior tests at the locus obtained under

5   comparable conditions.

34.   A method according to claim 12, wherein the
loci are selected on the basis of their ability to
discriminate among subjects.

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35.   A method, according to claim 3, wherein the
step A of reacting the material involves using a different
reaction from that of step A and the second allele is
different from the given allele.

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36.   A method according to claim 1, wherein step
(A) includes the step of assaying for the given allele using
genetic bit analysis.

20   37.   A method according to claim 1, wherein step
(A) includes the step of assaying for the given allele using
hybridization.

38.   A method, according to claim 1, wherein step
25   (A) includes the step of assaying for the given allele using
allele-specific amplification.

39.   A method, according to claim 1, wherein step
(A) includes the step of assaying for the given allele using
30   a polymerase chain reaction.

40.   A method, according to claim 1, wherein step

(A) includes the step of assaying for the given allele using a ligase chain reaction.

41. A method according to claim 12, wherein the loci are proximal to one another, so that the set of genotypes so produced may indicate a sequence of nucleotides associated with the genetic material.

42. A method of determining the genotype of a subject, the method comprising:

A. reacting genetic material taken from the subject at selected loci, each locus being an identified single nucleotide, to produce with respect to each of the selected loci a reaction value indicative of the presence of a given allele at each of the selected loci;

B. using the reaction values to determine the genotype of the subject and a confidence score, associated with the genotype being determined.

43. A method according to claim 42, wherein the loci are selected to provide information pertaining to inheritance of a trait.

44. A method according to claim 42, wherein the loci are selected to provide information pertaining to parentage of the subject.

45. A method according to claim 42, wherein the

5   loci are selected to provide information pertaining to the identity of the subject.

    46.   A method according to claim 42, wherein the loci are selected to provide information pertaining to

10   matching tissue of the subject with that of a donor.

    47.   A method according to claim 42, wherein the loci are spaced throughout the entire genome of the subject to assist in characterizing the genome of the species of the

15   subject.

add
B'

ADD
C'

ADD
D'